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Review Article

Gut Microbiota on Human Health, Disease and Attainment of the Human Gut Microbiota

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ABSTRACT

Over 100 trillion symbiotic microorganisms live on and within human beings and have a diverse function in human health and disease. But there are a variety of environmental and other factors that affect intestinal microbial dysbiosis, which has a close relationship with human health and disease. The pathogen microbes colonize intestinal mucosa this leading in the induction of a strong inflammatory response, followed by the translocation of the intestinal bacteria into other parts of the body. The imbalance of intestinal microbiota influences the production of immune mediators and stimulates both chronic inflammation and metabolic dysfunction. The wall of the bowel is highly permeable, and this leads to bacteria and/or endotoxin translocation, and it is an important stimulus for inflammatory cytokine that causes chronic heart failure. The variations of the microbiota are directly associated with the pathogenesis of other diseases, such as food allergies, severe asthma, autism, and depressive disorder. If the gut bacteria are maintained properly, they have varieties of benefits to the host, for example, regulation of gut motility, vitamin production, metabolizing xenobiotic substances, mineral absorption, removing toxins, genotoxins, and mutagens. Therefore, the aim of this review is to offers an up-to-date understanding of the effect of gut bacteria on human health and diseases.

Keywords: Symbiotic; Microbiota; Xenobiotic; Genotoxins; Colorectal

INTRODUCTION

Over 100 trillion symbiotic microorganisms live on and within human beings especially in guts and show an important role in human health and disease. The dysbiosis of intestinal microbes is affected by variety of environmental factors, which has a close relationship with human health and disease [1]. The human gut microbiota can carry genes 150 times more genes than are found in the whole human genome [2].

The gut microbiota has many vital functions in human health. Imbalance of the microbiota has been related to frequent intake of antibiotics and it is estimated for the increasing number of diseases. Now a day's studies have mostly focused on analysing the relationship between disease and an unusual microbiota composition. *In vitro* studies using gut models are required to evaluate the interactions that occur between specific bacteria or bacterial mixtures and gut epithelial cells. Studying the effect of oxygen requirement of gut microbiota in human gut epithelial cells is difficult because of most gut bacteria are obligate or facultative anaerobes [3]. Most known chronic diseases of human being are highly associated with the dysbiosis of gut microbiota. Such as, obesity, Inflammatory Bowel Disease (IBD), diabetes mellitus, metabolic syndrome, atherosclerosis, alcoholic and non-alcoholic liver and fatty liver disease (ALD), (NAFLD, cirrhosis, and hepatocellular carcinoma are highly related to imbalance of gut microbiota [4].

The microbiota has the mechanism to increase the extraction of energy from food, boost nutrient harvest and alter appetite signalling [5]. Versatile metabolic genes that contained in gut microbiota are found in the human genome which gives humans a unique and specific enzymes and biochemical pathways. Furthermore the gut microbiota are beneficial in nutrient acquisition or xenobiotic processing, as well as the metabolism of undigested carbohydrates and the biosynthesis of vitamins to the host [1]. The gut microbiota also offers a physical barrier, competitive exclusion of other or pathogenic microbes and producing lysis enzymes and antibiotic substances [1]. Moreover some bacteria in human gut such as Lactic acid bacteria used to reestablish the gut microbiota in patients that

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suffers from diarrhoea, following intake of frequent antibiotic that destroy the normal microbial flora in addition to their use as probiotics [6] (Figure 1).

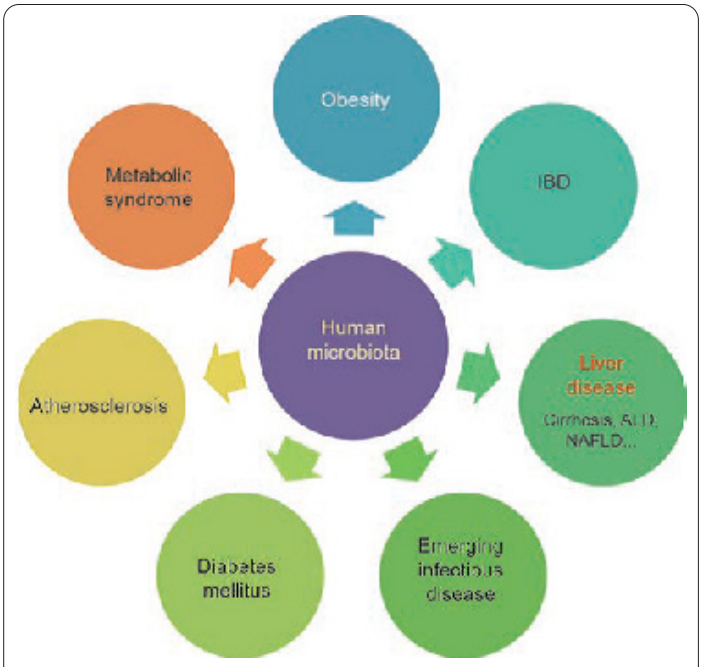

Figure 1: The relationship between human gut microbial symbiosis with diseases of different systems.

In this review, to provide a summary of the effect of the gut microbiota in human health and disease, the initiation of microbiome-wide association studies, and probable and important for the development of clinical applications for prevention and treatment of human diseases. Knowing the relationship between human health and gut bacteria can be useful for developing new probiotic treatments and novel ways in treating and controlling a wide variety of human diseases, and their pathogenicity while transit to other body parts.

THE DYSBIOSIS OF HUMAN GUT MICROBIOTA AND ITS DISEASE

Objective

The overall goal of this paper is to survey very surprising structures, systems and impacts of Plant Growth Promoting Bacterium (PGPB) on plant wellbeing and development improvement of Plant Growth

The gut microbiota and infectious diseases

Infection caused by imbalance of gut microbiota is one of the most common diseases. Infectious disease and its frequent treatment have a series impact on the gut microbiota, which in directly governs the outcome of the infectious disease in the human host [1]. As the aberrant pathogens colonize the intestinal mucosa, leads to the induction of a strong inflammatory response, followed by the translocation intestinal bacteria to other parts of bodies [1]. Many studies have confirmed the close relationship between infection and imbalance of the microbiota and shown the infection is associated not only with the bacteria, but also with viruses. For example, the intestinal microbiota of patients infected with *Clostridium difficile* (*C. difficile*) (CDI) is significantly altered [1]. The evolution of Human Immunodeficiency Virus (HIV), Hepatitis B Virus (HBV) and other diseases also disturbs the gut microbiota [7, 8].

Clostridium difficile Infection: The extreme overgrowth of *C. difficile* is generally related to frequent intake of antibiotic-associated diarrhea, is now a growing public health threat [9]. *C. difficile* is an obligate anaerobic, gram-positive rod, spore-forming that is one of the components of human gut microbiota. Frequent intake of antibiotics interrupts the intestinal mucosa homeostasis, these resulting in decreasing resistance against toxin-producing *C. difficile* and endorsing the progression of *Clostridium difficile* infection (CDI) [9]. Gu et al. evaluated that fecal bacteria diversity is decreased and the microbial composition intensely changes in patients following frequent administrations antibiotics. As studies showed, patients with frequent antibiotic treatment compared with healthy controls either CDI is present or not butyrate-producing anaerobic bacteria are drastically depleted [9]. Therefore changes or imbalance of gut micro biota communities can easily susceptible to *C. difficile* colonization. Gu et al. studied and evaluated that varies toxigenic *C. difficile* strains have varies effects on fecal bacteria in children [9]. Also, he evaluated that the strains of *C. difficile* that produce both toxin-A and toxin-B reduce fecal bacteria uniformity to a greater degree than strains of *C. difficile* that produce only toxin-B.

The impact of gut microbiota on *Helicobacter pylori*: *Helicobacter pylori* (*H. pylori*) are known to colonize the gastric mucosa and induces inflammation that causes peptic disease. Hu et al. evaluated the relationship of *H. pylori* infection with gum disease causing bacteria, tooth plaque bacterial pathogens, and inflammation. Their study showed that patients infected with *H. pylori* are highly colonized by *Porphyromonas gingivalis*, *Prevotella intermedia*, *Fusobacterium nucleatum*, and *Treponema denticola* than in those without H.pylori, on the other hand the incidence of Aggregatibacter actinomycete mcomitans bacteria in tooth is lower [8]. The outcome of the study shows that patients H.pylori may endorse the growth of some tooth plaque (periodontal) pathogens and intensify the progress of chronic periodontitis [8].

The effects of gut bacteria on HIV (Infection with HIV): Indigenous intestinal microflora has a symbiotic relationship with the intestinal mucosa and is an integral part of the gastrointestinal tract. Close interaction between the microbiota and mucosa is a major imperative of intestinal homeostasis [10]. It has been found out recently that dysbiosis changes in the gut (dysbiosis) accompany not only various intestinal disorders but are also associated with a wide range of multi-organ pathologies, including HIV infection. These factors lead to the penetration of lipopolysaccharide (LPS) and other bacterial components through the intestinal barrier into the blood circulation although bacteremia is not observed as a rule [11]. Translocation of LPS and chronic exposure to peripheral lymphocytes result in persistent systemic immune response accompanied by high level of pro-inflammatory cytokines, which fairly soon leads to the depletion of the immune system. It is believed that translocations and chronic immune activation play a significant in the development and progress on opportunistic complications [11]. Although it is not clear whether the dysbiosis of intestinal microbiota in HIV infection is a primary factor leading to the development of the disease or secondary response to other factors; it is evident that it leads to in the chronic phase of infection and the appearance of opportunistic complications [10].

HIV continues as one of global public health issues. Patients with HIV-1 are significantly increased with the *Firmicutes/Bacteroidetes* ratio and the gut bacteria is highly disturbed [9]. Even if the viral loads of HIV-1 are reduced following a short-term administration of Highly Active Anti-Retroviral Therapy (HAART), but the diversity and composition of the gut microbiota are not completely restored,

and the imbalance of gut bacteria continues [9].

The human gut microbiota and metabolic disorders: The diversity of the gut microbiota is affected by the frequent administration of antibiotics and by the lifestyle of the human host, including exercise, diet, and hygiene preferences. The imbalance of gut microflora affects the production of immune mediators and induces both chronic inflammation and metabolic dysfunction. The consequences of a complex interaction among host genetics, diet, environment, and the gut microbiota can cause obesity and its associated metabolic complications, such as type 2 diabetes (T2D) and cardiovascular disease [12]. However gut microbiota like Lactic acid bacteria can resist many antibiotics [13]. Isolated from traditional fermented and characterize Lactic acid bacteria in *in vitro* as probiotics and multiple drug resistance such as, resistance to penicillin, Levofloxacin and Oxacillin.

The effects of gut bacteria on obesity: Obesity is a medical condition in which an abnormal or excessive deposition of body fat that may impair health due to imbalance in energy consumption and expenditure. It has been linked with the dysbiosis of gut microbiota which may be either species or genus specific [12]. Age, lifestyle, wide range of feeding practice and geographical origin of the people may have an impact on microbial ecology of the human gut [12]. A difference in the composition of intestinal bacterial flora in obese and normal weight individuals seems to be a key factor in energy homeostasis. Another theory postulated to link obesity with gut microbiota is the production of short chain fatty acids like butylates, acetate and propionate from undigested polysaccharides. These compounds stimulate glucagon-like peptides which decrease gut motility allowing greater nutrients absorption. Research studies in mice demonstrated release of endotoxins like lipopolysaccharide (LPS) by intestinal flora on consumption of high fat diet. LPS is responsible for state of chronic low-grade inflammation, hence it is a link between gut microbiota and metabolic disturbances of obesity. Preclinical research results confirmed the role of intestinal microbiota in energy harvesting and storage. But such research findings in human being are in infancy stage [14]. However, some rumen bacteria have the ability to form Conjugated linoleic acid (CLA) which has an anti-obesity effect. These bacteria formulate the CLA from diets, such as beef, milk fat, natural, and processed cheeses, yogurt, and plant oil. Because of this the amount of CLA in human adipose tissue is depend on the dietary intake evaluated that six strains (four *Bifido*bacterium breve strains, a *Bifido*bacterium bifidum strain and a *Bifidobacterium pseudo-longum* strain) have the ability to produce verities of CLA and conjugated ⍺-linolenic acid isomers from free linoleic acid and ⍺-linolenic acid [15].

The effect of gut bacteria on diabetes type 2 (T2D): Many studies showed that gut microbiota is contributing to many human diseases including both diabetes type 1 and type 2. The association between the gut microbiome composition and the development of T2D is increasingly being uncovered [1]. Many studies showed that a dysbiosis of gut microbiome followed by lower diversity and resilience is directly associated with diabetes. The mechanisms the altered microbes that cause the disease by translocation of microbiota from the gut to the tissues and thus inducing inflammation evaluated that the human gut microbiome such as Prevotellacopri and *Bacteroides vulgates* may affect the serum metabolome and induce insulin resistance [1]. Nowadays there are promising strategies to reduce insulin resistance and related metabolic disease by ingestion of specific fibres or therapeutic microbes.

The effect of gut bacteria on autoimmune disease: The relationship between autoimmune diseases and the gut microbiome in humans were studied which shows the dysbiosis of microbiome causes an autoimmune disease. Restoring the balance of the gut bacteria can support to suppress the autoimmune system by activating different immune regulatory mechanisms. By stimulating the self-healing mechanisms, the affected individuals can prolong good health. Studied and evaluated that treating autoimmune diseases by using selective bacteria for controlling gut microbiota. There are different mechanisms for controlling gut bacteria such as, prebiotic diets, antimicrobial interventions, transplants of fecal microbiota, and choosing probiotics. Recent evidence has shown that the gut microbiota directly and indirectly modulates the host immune system.

The effects of gut bacteria on Inflammatory Bowel Disease (IBD): Crohn's Disease (CD) and Ulcerative Colitis (UC) are the two main types of inflammatory bowel disease that cause chronic and relapsing diseases that affects primarily young individuals and leading to serious damage of value of life. The pathogenesis of IBD is not fully clarified but it is commonly accepted that it is associated to an unfortunate stimulation of the gastro-intestinal immune system toward the gut microbiota in genetically susceptible hosts and under the influence of environmental factors [16].

The alterations in gut microbiota diversity induce imbalance between pro- and anti-inflammatory bacteria with possible functional consequences (Figure 2). For instance, *Faeca libacterium prausnitzii*, which is a major member of the *Firmicutes* phylum, has been shown to have anti-inflammatory effects both *in vitro* and in vivo. Therefore, low numbers of these bacteria in IBD patients' might be impact on inflammatory processes. On the other hand, as number of *Enterobacteria*, such as *Escherichia coli*, increased it might activate and fuel inflammation, especially adherent-invasive type of E. coli (AIEC) were specifically associated with the ileal mucosa that is about one third of CD patients are involved with ileal [16].

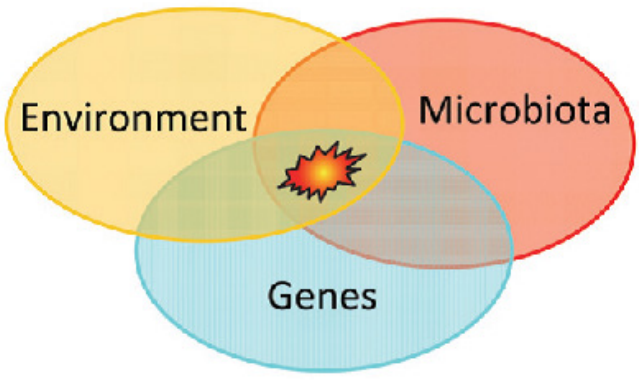

Figure 2: Three factors of IBD (Inflammatory Bowel Disease) pathogenesis.

The effect of gut microbiota on type 1 diabetes (T1D): Type 1 diabetes (T1D) is an autoimmune disease that is caused by the destruction of pancreatic β-cells by the immune system. T1D is mainly caused by genetic defect, in addition to this epigenetic and environmental factor also have been shown to play an important contribution for this disease. In recent years higher rates of T1D incidence have been not reported only by genetic factors but also in the changes of our lifestyle such as diet, hygiene, and antibiotic usage that can directly affect the gut microbiota [1].

Gut microbiota and rheumatoid arthritisC

Rheumatoid Arthritis (RA) is a systemic, inflammatory, and chronic disease determined by an insistent immune response that causes inflammation and destruction of joints. Characterization of gut microbiota recently increased instead of a wide research field, particularly in autoimmune diseases. Gut microbiota is rich in microbes that have beneficial as well as pathogenic effects on human health. As recent studies showed Intestinal bacteria play a role as mediator of inflammation. Studies have shown that intestinal microbiota on rheumatoid arthritis is characterized by an increase or decrease of bacterial groups as compared to controls and studies on the impact of intestinal bacteria on rheumatoid arthritis and evaluated that gut microbiomes influence immune response in and away from the gut by varying the gut permeability and immunity. Imbalance of bacteria helps the growth of rheumatoid arthritis related bacteria and reduces the beneficial bacteria.

The effects of gut bacteria on liver disease: Gut microbiotas play a key role to maintain communication between the gut and liver health. The gut microflora produces substances like ethanol, ammonia, and acetaldehyde which are metabolized by the liver and also control Kupffer cell activity and cytokine production [15]. Therefore, massive growth of bacteria in small intestine may be an important pathogenesis of Non Alcoholic Steato Hepatitis (NASH). The movement of Small intestine was decreased by massive growth of bacteria in NASH rats. The severity of this can be decreased by antibacterial treatment [17]. The intestinal permeability and endotoxin translocation can be increased by the alternation of intestinal bacteria both in quantitative and qualitative. As a result, the action induces the transcriptional activation of quite a lot of pro-inflammatory genes and cytokines in the liver. The study showed translocated intestinal bacteria could cause spontaneous bacterial peritonitis in cirrhotic rats, which aggravated cirrhosis [17]. The urease-positive bacteria which produce ammonia from amino acids by deamination which causes a dreaded Hepaticen cephalon pathy (HE). Which is an important critical factor in pathogenesis of HE. The Treatment of this disease is more effective by probiotics than prebiotics and antibiotics [15].

The effects of gut bacteria on heart disease: Even if there are continuous advances in treatment options, cardiovascular diseases (CVDs) keep on the leading cause of death in the world. Microbes that are translocated from the gastrointestinal tract (GIT) for a long time are considered as a normal phenomenon imperative for the microbial maturity of the GIT in both healthy humans and diseased individuals [18]. However, in recent studies the increased microbial translocation has an impact in the clinical complications of systemic inflammatory diseases and surgically treated individuals has gained more importance in the past decades. Dinakaran evaluated on systemic disease and concludes that microbes have more impact particularly in 'immunologically privileged' sites of the human body [18].

Many studies showed that the colonization of intestinal mucosa with Lactobacillus brevis has lower bowel permeability, whereas colonization with *E.coli, Klebsiella pneumonia*, and *Streptococcus viridians* showed higher permeability [15] studied and suggested that a bowel wall with high permeability may lead the bacteria for endotoxin translocation; this may be an important stimulus for inflammatory cytokine to be stimulated in chronic heart failure

The effects of human gut microbiota on cancer: Gastrointestinal cancer is one of the leading killer diseases in the world. In recent studies besides the genetic factors, the residential microbes in the GIT (non-genetic factors) is one of gastrointestinal cancer risk. Current studies in microbial research on GI malignancies, for example gastric cancer, colorectal cancer, and esophageal cancer, give a clue into the role of the human microbiota in carcinogenesis.

Gastric cancer and gut microbiota: Chronic inflammation caused *H. pylori* is considered to be one of risk factor for gastric cancer studied on gastric cancer and evaluated that per year, approximately 660,000 new cases of gastric cancer are caused by *H. pylori* infection, and this results in the loss of acid-producing parietal cells, development of gastric atrophy, metaplasia, dysplasia, and, finally, carcinoma formation [1]. The elimination of H. pylori before the beginning of chronic atrophic gastritis may protect against gastric cancer. World Health Organization (WHO) also classified as class I carcinogen [19]. Investigated that the carcinogenic risk may be related to the genetic variety of the *H. pylori* strain, variations in host responses, and specific host-microbe interactions. Significantly, the phylogenetic origin of *H. pylori* is a good predictor of the risk for gastric cancer.

Colorectal cancer and gut microbiota: Recent studies showed that the imbalance of gut microbiota has a significant impact on the interactions of the gut microbiome and the development of colon cancer [20]. Different studies on microbiota in cases of CRC is categorized by a high proportion of potential pathogens, for instance *Pseudomonas, Helicobacter*, and *Acinetobacter*, and a lower richness of beneficial bacteria, such as butyrate-producing bacteria [20]. They also, observed that the gut microbiota from tumor-bearing mice promotes inflammation and tumor genesis in recipient animals, thus directly contributing to CRC. However, it is still not clear from human studies whether the dysbiosis in the microbial community is a cause or consequence of adenomas and CRC.

Esophageal cancer and gut microbiota: Esophageal cancer is a cancer that happens in the esophagus that rounds from our throat to stomach. As current studies confirmed the chronic inflammation at the termination of the esophagus and esophageal adenocarcinoma (EA) are closely related which is caused by gastro esophageal reflux. Therefore, the whole process of the disease can be described as "gastro esophageal reflux disease–Barrett's esophagus–esophageal adenocarcinoma" (GERD–BE–EA). So, as researchers suggested the cause of morbidity in the world by EA may be associated with the regular use of antibiotics. Also, many studies have stated that patients with GERD are more related with micro ecological changes. Yet, the resident microbiome does not differentiate between squamous cell carcinoma and adenocarcinoma [1]. Moreover, the contribution of *H. pylori* in the development of disease of GERD and EA is still vague and controversial. In addition, researchers have found that, with the decline in H.pylori infection, GERD incidence has increased [1]. Wang also suggested that *H. pylori* may contribute for a protective role in the development of GERD and associated EA. Yet, the avoidance of *H. pylori* treatment does not degenerate GERD or increase new GERD

The human gut microbiota on varies diseases: As many researchers evaluated the dysbiosis of the gut microbiota are the cause of development of many other diseases, for instance, food allergies, severe asthma, and autism, are the main, but these diseases may not involve straight interactions with the microbiota [21].

The impact of gut microbiota on allergic diseases: A number of studies showed that a consumption of antibiotics during early life,

causing low diversity of gut microbiota which enhances susceptibility to allergic asthma, and therefore may also affect asthma occurrence in child hood after continuing follow-up. The gut microbiota composition also affected by the mode, place of delivery, and infant feeding and subsequently, this influence the risk of atopic manifestations [21]. The study on infant gut microbiota found that at age of 3–6 months *Clostridia* and *Firmicutes* are dominant these are associated with Cow's Milk Allergy (CMA) and resolved at age of eight. And also, they found that the cause CMA in childhood is because of the rapid evolvement of the intestinal microbiota in the first year. The gut microbiota and immune system associates closely, which gives signals to indorse the maturation of regulatory antigen-presenting cells and regulatory T cells (Tregs), which play a vital role in the progress of immunological tolerance, for instance, the members of the *Clostridium* species interact with Treg and control immunoglobulin E (IgE) levels [21].

The effect of gut microbiota on autism: Autism spectrum disorders (ASDs) are disorders of neurodevelopmental that are categorized as stereotyped behaviours, cognitive and social skills impairments [15]. The maintenance of normal brain and GI function is determined by gut-brain axis found that the critical regulator of gut-brain axis was gut microbiota [1]. The disease of autism is caused by intestinal bacteria. The drug vancomycin (for gram positive bacteria) and metronidazole (for both gram negative and gram positive), are the drug of choice for the treatments of individuals with ASDs, although vancomycin is not absorbed from the gastrointestinal tract. In ASD patients there is an increase of *Clostridia* and a decrease in *Bifido*bacteria were involved, because *Clostridium* produces exotoxins and propionate, the worsened ASD-like behavior Autistic (AD). Because, children have a distinct and less diverse gut microbial community structure, and showed significantly lower levels of genera *Prevotella, Coprococcus,* and unclassified *Veillonellaceae* [15]. Experimental studies on two organisms (*Bacteroides vulgates* and *Desulfo vibrio* species, including *D. desulfuricans, D. fairfieldensis*, and D. piger) and were found that more commonly found in stools of AD children than in the control children's stools also, found that *Firmicutes* and *Actinobacter* were less of the total flora of AD children's stools than the control children's stools [22].

The human microbiota in health

The composition and function of gut microbiota vary based on different in sites, ages, sexes, races, and diets of the host [23]. The recent study shows to obtain particular compounds by using microbial metabolism as chemical machinery on food/feed fermentation technology need processed design. Therefore, LAB fermentation is not used only for starting food material and economic importance but, it increases food/feed production and promotes human health in the world [6].

Gut bacteria and immune system

The development of the humoral and cellular mucosal immune system is stimulated by colonization of gut bacteria. The innate immune system of the hematopoietic and non-hematopoietic cells is used to sense the signals and metabolites of microorganisms and translated into physiological responses. Researchers also studies by comparing normal mice with germ free mice (GM) and found that the occurrence of gut-associated lymphoid tissue and antibody production were show extensive defects on germ free mice [24]. This study has also confirmed that the gut microbiota used to generate a tolerogenic response performs on gut dendritic cells and inhibits the type 17 T-helper cell (Th17) anti-inflammatory pathway [24]. However, some gut microbiota also induces inflammation in a certain condition in addition to their health benefits. Pathogen-associated molecular patterns that are found in the bacterial cell wall such as, Lipopolysaccharides (LPSs) and peptidoglycan (PGN) are used to activate and induce individually or synergistically the nuclear factor κB (NF-κB) effectors and the production of inflammatory cytokines such as tumor necrosis factor α (TNF-α), interleukin 1β (IL-1β) and antimicrobial peptides in the defence against foreign pathogens respectively [15]. Also, regular consumption of fermented foods containing LAB boosts the immune system and strength then the body. Indirectly that fights against pathogenic bacterial infections (Figure 3). LAB also used for the production of bacteriocins which is a potential drug candidate for replacing antibiotics in order to treat multiple drug resistance pathogens in the future [6].

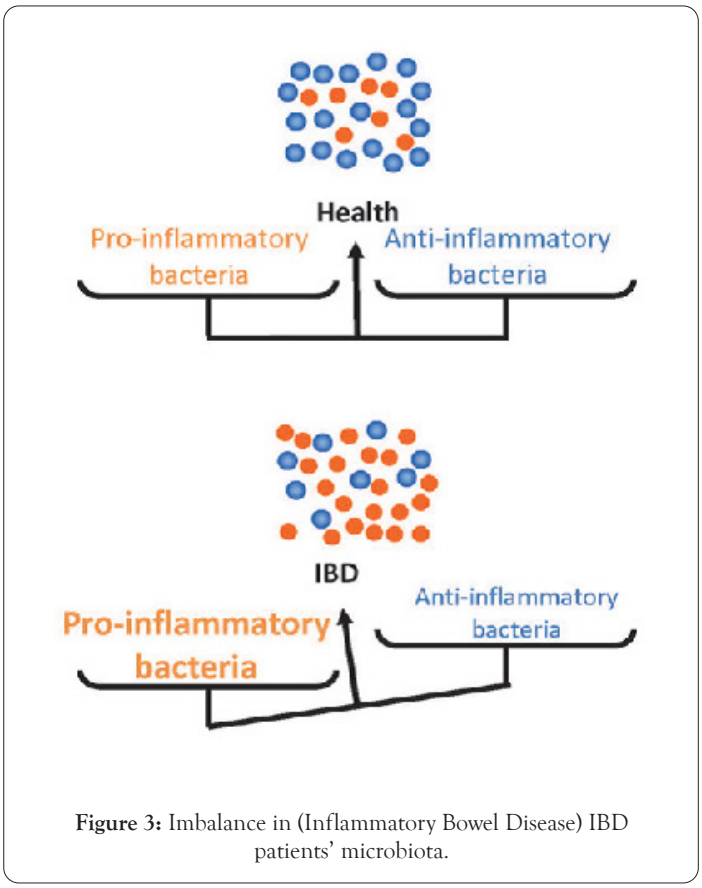

Figure 3: Imbalance in (Inflammatory Bowel Disease) IBD patients' microbiota.

Benefit of gut bacteria to the host

The gut bacteria benefit in a different way to the host if they are distributed/colonized in balance, for instance, it maintaining/regulating gut motility, synthesis of vitamins, transforming bile acid and steroids, breakdown of xenobiotic substances, absorbing minerals, and stimulating and removing toxins, genotoxins, and mutagens. Also, a great amount of short-chain organic acids, such as acetic, propionic, and butyric acids are produced in proximal region of colon. Theses organic acids used for the colonic mucosa and peripheral body tissues as energy sources, and they are metabolites of undigested complex carbohydrates which are fermented by colonic bacteria [15]. In directly, the bacterial growth in the colon is affected by these organic acids, by lowering faecal pH and affecting colonic water absorption [15]. Gut symbiotic bacteria used for varies purposes such as, degrade/digest indigestible compounds, giving essential nutrients, protect against occupation

by opportunistic pathogens, and it has played a role to the formation of intestinal architecture. For example, undigested certain foods by small intestine and stomach is digested by the intestinal microbiota and also contributes in maintaining energy homeostasis. Specific species of Bacteroides are used to digest fiber containing foods; these foods are primarily dietary fibers such as xyloglucans, which are usually found in vegetables. Lactobacillus and *Bifido*bacterium are also used to utilize other non-digestible fibers, such as fructo-oligosaccharides and oligosaccharides [25].

Acquisition of the human gut microbiota

During birth the human infant gut is free from any microbes and attains its own microbiome, and the transition to bacterial population equilibrium with in the days and weeks following delivery, the population of microbe's early-in-life quietly influences later-in-life host biology. The procedures of colonization of human gastrointestinal tract after birth are a fascinating example of ecological succession, even a process is not studied well. By explaining the dynamics of the de novo assemblage of this microbial community we could gain a better understanding as to how the gut attains its formation microbiome, the first step in the process to population equilibrium [26].

Meconium: The meconium is a lacking of microorganisms at birth [27]. However, this dogma is reconsidered after several reports over the past decade have provoked us [28]. Specifically, the viable bacteria are contained in freshly passed meconium and cord blood. Also, there is evidence that amniotic fluid and placenta have a microbial colonization, even in the absence of premature rupture of the membranes. Yet, it is important to note that DNA sequences are more commonly identified than are viable bacteria [29]. There has also been substantial attention paid to amniotic infection/colonization and preterm labour, but the role of bacteria within fetal membranes in causing preterm labour needs further work before this connotation should be considered to be established [30].

The first colonizers of gut microbiota in life span of infants

The sequential phases of bacterial colonization in life span of infants were studied and have presented. But these studies face challenges, mainly because it is very difficult to obtain stool samples at high frequencies from infants exist in with their families in the community, and sequencing methodologies and sampling differs greatly between studies. A number of gut microbes present in adult population does not occur until about three years of age. The concentration of gram negative bacteria becomes higher in the stools of older children and adults [31]. Anaerobes are well represented members of the gut microbiota within several days of birth [32]. The change in diary shifts gut microbial population, and initial feeding choice (breast milk or formula) had persistent effects [33].

Infant microbial gut content depends on maternal body habitus: The higher concentrations of fecal Bacteroides, *Clostridium*, and *Staphylococcus* genera, the higher maternal body mass index and normal body mass indices of mother, the lower densities of *Bifido* bacteria. *Akkermansia muciniphila, Staphylococcus spp*. and *Clostridium difficile* [30].

Mode of delivery and infant gut microbiota: The colonization of infant gut by bacteria during delivery is originated from vagina or skin if it is born vaginally or *via* caesarian section, but the number of mother-infant studied is still quite limited. When, infants born *via* vaginal delivery have a more rapid in-flux of *Proteobacteria* (Gram-negative organisms), and a higher proportion of *Bifido* bacteria multiple species, but particularly (*catenulatum* and *longum*) than those born *via* Caesarian section. The concentration of gut bacteria of infants that are born *via* Caesarian section during four months of age, are under-represented in *E.coli* and Bacteroides spp. [34].

The impacts of gut bacteria on early-in-life colonization on successive well-being of the host: As epidemiological evidence suggests that the development of asthma and Inflammatory Bowel Disease is caused by early-in-life exposures to microorganisms [35]. The densities of *Lactobacilli* in the stool are lower in the human with allergies at age five years in early infancy than children without allergies. Domination of *C. difficile* in the first month of life is associated to atopy and at age six years related to asthma. The of *Staphylococcus species, E. coli* and *Bacteroides* in stools in the first several months of life were related with expected childhood body mass (weight for age Z-scores) at up to 24 months of age [36].

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CONCLUSION

This review is to give recent understanding of the impact of gut bacteria in human health and diseases. Many diseases, like IBD, obesity, diabetes, carcinoma, HIV, and autism are caused by the dysbiosis of bacteroides in the gut. To know the role of gut bacteria on disease and to discover the exact pathogenesis, further studies should be carried out. For the maintenance of normal colon cells, reduction of proliferation and activate apoptosis of human colon carcinomas butyrate shown to be quite an important nutrient. To identify the bacteria that are producing butyrate additional studies should be carried out. Also, the benefit of mixed prebiotics and probiotics on human health should be further investigated. Because the effect of gut bacteria is important on human health and diseases, they can be used as a new target to prevent and treat many chronic diseases, and future studies are guaranteed to target them in varieties of ways to counter attack the gut bacteria-related diseases.

REFERENCES

1. Wang B, Yao M, Lv L, Ling Z, Li L. The human microbiota in health and disease. Engineering. 2017; 3: 71-82.
2. Ursell LK, Haiser HJ, Van Treuren W. The intestinal metabolome: An intersection between microbiota and host. Gastroenterology. 2014; 146: 1470-1476.
3. Martels JZ, Sadabad MS, Bourgonje AR. The role of gut microbiota in health and disease: *In vitro* modeling of host-microbe interactions at the aerobe-anaerobe interphase of the human gut. Anaerobe. 2017; 44:3-12.
4. Wang B, Jiang X, Cao M. Altered fecal microbiota correlates with liver biochemistry in nonobese patients with non-alcoholic fatty liver disease. Scientific Reports. 2016; 6: 32002.
5. Perry RJ, Peng L, Barry NA. Acetate mediates a microbiome–brain–β-cell axis to promote metabolic syndrome. Nature. 2016; 534: 213.
6. Admassie MA. Review on food fermentation and the biotechnology of lactic acid bacteria. World J Food Sci and Technol. 2018; 2: 19.
7. Cohen J. Vaginal microbiome affects HIV risk. In: American Association for the Advancement of Science. 2016; 353 (6297): pp 331.
8. Hu Z, Zhang Y, Li Z. Effect of *Helicobacter pylori* infection on chronic periodontitis by the change of microecology and inflammation. Oncotarget. 2016; 7:66700.
9. Gu S, Chen Y, Zhang X. Identification of key taxa that favor intestinal colonization of *Clostridium difficile* in an adult Chinese population. Microbes and Infection. 2016; 18: 30-38.
10. Gorobchenko K. Effects of probiotics on intestinal microflora of HIV-infected individuals. J Advances in Microbiol. 2017; 1-7.
11. Saxena D, Li Y, Yang L. Human microbiome and HIV/AIDS. Current HIV/AIDS Reports. 2012; 9: 44-51.
12. Sanz Y, Santacruz A, Gauffin P. Gut microbiota in obesity and metabolic disorders. Proceedings of the Nutrition Society. 2010; 69: 434-441.
13. Akalu N, Assefa F, Dessalegn A. *In vitro* evaluation of lactic acid bacteria isolated from traditional fermented Shamita and Kocho for their desirable characteristics as probiotics. African Journal of Biotechnology. 2017; 16: 594-606.
14. Pedersen R, Ingerslev H-C, Sturek M. Characterisation of gut microbiota in Ossabaw and Göttingen minipigs as models of obesity and metabolic syndrome. PLOSOne. 2013; 8: e56612.
15. Zhang YJ, Li S, Gan RY, Zhou T, Xu DP, Li HB. Impacts of gut bacteria on human health and diseases. Internat J Molecular Sci. 2015; 16: 7493-7519.
16. Cammarota G, Ianiro G, Tilg H. European consensus conference on faecal microbiota transplantation in clinical practice. Gut. 2017; 66: 569-580.
17. Gottardi A, Mccoy KD. Evaluation of the gut barrier to intestinal bacteria in non-alcoholic fatty liver disease. J hepatology. 2011; 55:1181-1183.
18. Dinakaran V. Microbial translocation in the pathogenesis of cardiovascular diseases: A microbiome perspective. J Cardiol Curr Res. 2017; 8.
19. Sablet T, Piazuelo MB, Shaffer CL. Phylogeographic origin of *Helicobacter pylori* is a determinant of gastric cancer risk. Gut. 2011; 60: 1189-1195.
20. Hansen AK, Nielsen DS. Handbook of Laboratory Animal Bacteriology. CRC Press. 2014.
21. Bunyavanich S, Shen N, Grishin A. Early-life gut microbiome composition and milk allergy resolution. J Allergy and Clinical Immunology. 2016; 138: 1122-1130.
22. Heberling CA, Dhurjati PS, Sasser M. Hypothesis for a systems connectivity model of autism spectrum disorder pathogenesis: Links to gut bacteria, oxidative stress, and intestinal permeability. Medical Hypotheses. 2013; 80:264-270.
23. Hollister EB, Gao C, Versalovic J. Compositional and functional features of the gastrointestinal microbiome and their effects on human health. Gastroenterology. 2014;146,:1449-1458.
24. Magrone T, Jirillo E. The interplay between the gut immune system and microbiota in health and disease: Nutraceutical intervention for restoring intestinal homeostasis. Current Pharmaceutical Design. 2013; 19:1329-1342.
25. Goh YJ, Klaenhammer TR. Genetic mechanisms of prebiotic oligosaccharide metabolism in probiotic microbes. Annual Review of Food Science and Technology. 2015; 6:137-156.
26. Yatsunenko T, Rey FE, Manary MJ. Human gut microbiome viewed across age and geography. Nature. 2012; 486: 222.
27. Tissier H. Recherches sur la flore intestinale des nourrissons: (état normal et pathologique). 1900.
28. Funkhouser LJ, Bordenstein SR. Mom knows best: The universality of maternal microbial transmission. PLOS Biology 2013; 11: e1001631.
29. Rautava S, Collado MC, Salminen S, Isolauri E. Probiotics modulate host-microbe interaction in the placenta and fetal gut: A randomized, double-blind, placebo-controlled trial. Neonatology. 2012; 102:178-184.
30. Collado MC, Isolauri E, Laitinen K, Salminen S. Effect of mother's weight on infant's microbiota acquisition, composition, and activity during early infancy: A prospective follow-up study initiated in early pregnancy. The American J Clinical Nutrition. 2010; 92: 1023-1030.
31. Saulnier DM, Riehle K, Mistretta TA. Gastrointestinal microbiome signatures of pediatric patients with irritable bowel syndrome. Gastroenterology. 2011;141: 1782-1791.
32. Jost T, Lacroix C, Braegger CP, Chassard C. New insights in gut microbiota establishment in healthy breast fed neonates. 2012; 7: e44595.
33. Fallani M, Amarri S, Uusijarvi A. Determinants of the human infant intestinal microbiota after the introduction of first complementary foods in infant samples from five European centres. Microbiology. 2011; 157: 1385-1392.
34. Azad MB, Konya T, Maughan H. Gut microbiota of healthy Canadian infants: Profiles by mode of delivery and infant diet at 4 months. Cmaj. 2013;185: 385-394.
35. Ege MJ, Mayer M, Normand A-C. Exposure to environmental microorganisms and childhood asthma. New England J Medicine. 2011; 364: 701-709.
36. White RA, Bjørnholt JV, Baird DD. Novel developmental analyses identify longitudinal patterns of early gut microbiota that affect infant growth. PLOS Computational Biology. 2013; 9: e1003042.